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Result
No.
                                                                                                                                                                                                                                                                                                                                                                     Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 SwissProt_40:*
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Listing first 45 summaries
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                            SM3C_HUMAN
SM4F_MOUSE
SM3C_CCHICK
SM4B_HUMAN
SM4C_MOUSE
SM3D_CHICK
SM4G_HUMAN
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SM3E_MOUSE
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2442.495 Million cell updates/sec
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Semaphorin 7A precursor (Semaphorin L) (Sema L)
K1) (CD108 antigen) (CDw108).
SEMA7A OR SEMKI OR SEMAL OR CD108.

(Semaphorin K1) (Sema

Q9QUR8; 088371; SM7A_MOUSE

STANDARD;

PRT;

664

Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;

Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Murinae; Mus

Mus musculus (Mouse)

TISSUE=Brain; SEQUENCE FROM N.A.

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SM7A_MM
SM7A_M
AC Q9QUR8
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT SEMA7A
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OC ENTATY
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                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- TISSUE SPECIFICITY: HIGHEST EXPESSION IN BRAIN. LOWER IN HEART,
-THYMUS, SPLEEN, TESTIS AND OVARY. THE EXPRESSION INCREASES IN LA
EMBRYONIC AND POSTNATAL STAGES.
-!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
-!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
-!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CDw108 expression during T-cell development.";
Tissue Antigens 55:429-436(2000).
-!- FUNCTION: MAY PLAY AN IMORTANT ROLE IN THE NERVOUS
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STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=20340072; PubMed=10885563;
Mine_T., Harada K., Matsumoto T., Yamana H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98389619; PubMed=9721204;
Lange C., Liehr T., Goen M., Gebhart E., Fleckenstein B., Ensse
"New eukaryotic semaphorins with close homology to semaphorins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99096477; PubMed=9878861;
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Best Local :
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                                                                                                  075326;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-7001 (Rel. 40, Last annotation update)
Semaphorin 7A precursor (Semaphorin L) (Sema L) (Semaphorin K1) (Sema K1) (John-Milton-Hargen human blood group Ag) (JMF group antigen) (CD108 antigen) (CDw108).
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CARBOHYD
CONFLICT
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DISULFID
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                                                                                                                                                                                SM7A_HUMAN
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AF030699;
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SM00423; PSI; 1.
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Pred. No. 1.8e-172;
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CELL ATTACHMENT SITE (I
GPI-ANCHOR (POTENTIAL)
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99344620; PubMed=10416131;
Angelisova P., Drbal K., Cerny J., Hilgert I., Horejsi V.;
"Characterization of the human leukocyte GPI-anchored glycoprotein
CDw108 and its_relation_to_cher similar molecules.";
                                                                                                                 Signal;
                                                                                                                                          SMART;
                                                                                                                                                                                                                      EMBL; AF069493; EMBL; AF071542;
                                                                                                      Developmental
                                                                                                                                SMART;
                                                                                                                                                         Pfam; PF01403; Sema;
                                                                                                                                                                  InterPro; IPR003599; Ig.
InterPro; IPR003659; Plexin-like
InterPro; IPR001627; Sema.
                                                                                                                                                                                                         Genew; HGNC:1074
                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human semaphorin K1 is glycosylphosp
defines a new subfamily of viral-rela
J. Biol. Chem. 273:22428-22434(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98380463; PubMed=9712866; Xu X., Ng S., Wu Z.-L., Nguyen D., Ebens A., Luo Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning CDw108.";
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Sagawa K.,
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MEDLINE=99218431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunobiology 200:234-245(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION
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"New eukaryotic semaphorins
                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Attached to the membrane by a GPI-an TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, TESTIS, OVARY, BRAIN, SPINAL CHORD, LUNG, HERRT, ADRENAL GLAND, LYMPH NOD THYMUS, INTESTINE AND KIDNEY.

SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunol.
                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT
                                                                                                                ; SM00409; IG; 1.
; SM00423; PSI; 1.
1; Immunoglobulin
                                                                                                                                                                                                                                              AF030697;
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                                                                                                                                                                                                                                                                                                                                                  the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kubo K., Takeshita T.
Sugamura K., Itoh K.;
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559
5648
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                                                                                                                                                                                                                                                                                                                                                  Swiss Institute
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                                                                                                      protein;
                                                                                                                                                                                                                     AAC34261.1; -... AAC34741.1; -... AAC82642.1; -... AAC80456.1; -...
                                                                                                                                                                                                                                                                                                                                                 entry is copyright. It is produced through iss Institute of Bioinformatics and the EN
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                                                                                                      Glycoprotein;
                                                                                                                 domain; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosylphosphatidylinositol-linked
of viral-related semaphorins.";
REMOVED IN MATURE FORM (
SEMA.

IG-LIKE C2-TYPE DOMAIN.

CELL ATTACHMENT SITE (PC
GPI-ANCHOR (POTENTIAL).

BY SIMILARITY.
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                                                                             SEMAPHORIN
                                                                                          POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROLE IN THE NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homburger
                                                                                                      GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ., Fleckenstein B., Ensser A.; homology to semaphorins of DNA
                                                                             7 A
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                                                                                                                  Neurogenesis;
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                          (POTENTIAL)
                                                                (POTENTIAL)
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Matches 358
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30-MAY-2000
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CARBOHYD
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                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
STRAIN-C57BL/6; PubMed-8969198;
MEDLINE-97125976; PubMed-8969198;
Furuyama T., Inagaki S., Kosugi A., N.
Iwahashi Y., Miyazaki N., Hamaoka T.,
                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Semaphorin 4D precursor (Semaphorin J) (Sema
                                                                               "Identification of a lymphocytes.";
J. Biol. Chem. 271:33
                                                                                                                                                                                                                                                        MOUSE
                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                      Mus musculus (Mouse
Eukaryota; Metazoa;
                                                                                                                                                                                     (M-Sema G).
SEMA4D OR SEMAJ OR SEMACL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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            BIOL Chem. 271:33376-33381(1996).

BIOL CHEM. 271:33376-33381(1996).

FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE IMMUNE S AS IN THE NERVOUS SYSTEM.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LYMPHOID T ESPECIALLY IN THE THYMUS, AS WELL AS IN THE NERVOUS SYMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.

SIMILARITY: CONTAINS 1 SEMA DOMAIN.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE I SIMILARITY: CONTAINS 1 SEMA DOMAIN.
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SWISS-PROT entry
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EMBL; U69535; AAC52964.1; -. MGD; MGI:109244; Sema4d.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001627; Sema.
Pfam; PF00403; Sema; 1.
Pfam; PF01403; PSI; 1.
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European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                                        TFLKAMLVCSDAATNRNFNRLQDVFLLPDPSGQWRDTRVYGVFS---
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                                                                   SFLKARLICSKPDSGLVFNILQDVFVLRAPG--LKEPVFYAVFTPQLNNVGLSAVCAYTL
                                                                                                                                                                                                                                                                              CAEKGKSKQTECLNYIRVLQPLSSTSLYVCGTNAFQPTCDHLNLTSFKFLGKSEDGKGRC
                                                                                                                                                                                                                                                                                                                  CQDK----
                                                                                                                                                                                                                                                                                                                                                                                                                      RMCAPVRGLFLALVVVLRTAVAFA-----PVPRLT--WE-----HGEVGLVQFHKPG
ATVEAVFSRGKYMQSATVEQSHTKWVRYNGPVPTPRPGACIDSEARAANYTSSLNLPDKT
                                                                                                                                      ADVIQKSPDGPEGEDDKVYFFFTEVSVEYEFVFKLMIPRVARVCKGDQGGLRTLQ-KKWT
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SM00423; PSI; 1.
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29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin
                                  RTSSLK - - GYHMGLSNPRPGMCLPKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE C2-TYPE DOMAIN.
BY SIMILARITY.

N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 389.5;
Pred. No. 3e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n domain; Multigene Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5; DB 1;
3e-25;
ches 151;
                                                                                                                                                                                                                                                                                                <u>::</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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                                  PIPTET
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                                                                                                     337
                                                                                                                                                                        280
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SASSULT

OCCORDER RESULT

OCCOR
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SEQUENCE FROM N.A.

MEDLINE=96210603; PubMed=8633026;

Sekido Y., Bader S., Latif F., Chen J.-Y., Duh F.-M., Wei M.-n.,

Albanesi J.P., Lee C.-C., Lerman M.I., Minna J.D.;

"Human semaphorins A(V) and IV reside in the 3p21.3 small cell lung

cancer deletion region and demonstrate distinct expression patterns

na+1. Acad. Sci. U.S.A. 93:4120-4125(1996).
                             DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                        Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM3B_HUMAN STANDARD;
CJ3214; Q93018;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Cast annotation update)
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1. Pfam; PF01403; Sema;
                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS (BY
                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U28369; 
EMBL; U73167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEMA3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: SECRETED (BY SIMILA ENDOPLASMIC RETICULUM.
TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY VARIETY OF NEURAL AND NONNEURAL TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
                                                                                                                                                                                                                                                                                                    SM00409; IG;
SM00423; PSI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC: 10724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR SEMA5
                                                                                                                                                                                                                                                                          Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                       IPR003599; Ig.
IPR003006; Ig_MHC.
IPR003659; Plexin-like.
IPR001627; Sema.
29
749
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                                                                                                                                                                                                                                                                               domain;
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         ₹.
                  SEMA.

IG-LIKE C2-TYPE DOMAIN.

POLY-GLY.

POLY-GLY.

ARG-RICH (BASIC).

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

PRLRISEO -> HARGSPSKY (IN REF. 2).
                                                                                                                                                                                                                                 SEMAPHORIN
                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                                          Multigene family; Glycoprotein.
      1F3B8F63F59444F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no rest
                                                                                                                                                                                                                                   3B.
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      CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                      SEQUENCE OF TOWNS AND THE COMPLEX G.;
ROHLFING T., Tin Wollam A.M., Duckels G.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL COMES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWT COMES. COULD SERVE AS A LIGAND THAT GUIDES TO THE COMPLEX
           <del>: :</del>
                                                                                                                                                                                     Cell
                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                      Submitted
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                       SEMA3A.
                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                  Q14563;
30-MAY-2000
                                                                                                             SEQUENCE
                                                                                                                                                                                                            "The semaphorin genes encode
                                                                                                                                                                                                                                                                                                                                                Semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                            SM3A_HUMAN
                                                                                                                                                 Woessner
                                                                                                                                                                                                                                   TISSUE=Fetal brain;
MEDLINE=94094332; P
                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398
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                                                                                                                                                           genes encode a family o. ..... cone guidance molecules."; 11 75:1389-1399(1993).
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        BY A MOTILITY-INHIBITING MECHANISM. BINDS NEUROPILIN-1/PLEXIN-1 (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted (By similar DOMAIN: STRONG BINDING TO NEUROPILIN IS ME
THIRD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIQFARNHPLMYNSVLPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFQVADSHPEVAQRVEPMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSAAPSPPRLRL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAAPSAPRARVLSLPARFGLPLRLRLLLVFWVAAASAQGHSRSGPRISAVWKGQDHVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPYPRPGMC-PSKTFGTFSSTKDFPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCVYSLGDIDRVF-----RTSSLKGYHMGLSNPRPGMCLPKK-----QPIPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKWTTFLKARLVCSVPGVEGDTHFDQLQDVFLL--SSRDHRTPLLYAVFSTSSSIFQGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRSL-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPQFIKA-TIVHQDQAYDDKIYYFFREDNPDKNPE-APLNVSRVAQLCRGDQGGESSLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDGKGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDIGT----ECMNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STKGSCQDKQDCGNYITLLER-RGNGLLVCGTNARKPSC----WNLVNDSVVM----SL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERTCCYQALLVDEERGRLFVGAENHVASLNL---DNISKRAKKLAWPAPVEWREECNWAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQPEPHTVLFHEPGSFSVWVGGRGKVYHFNFPEGKNASVRTVNI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                               OF 39-182 FROM
T., Tin-Wollam
                                                                                                                                                 J., Minx P., Hind
                                                                                                                                    (MAR-1998) to the
                                                                                                                                                                                                                                                                                                                                                 3A
THE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                precursor
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                   PubMed=8269517;
                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
28
                                                                                                                                                 Hinds
                                                                                                            N.A.
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                                                                                                                                                                                                                                                                                                                                                (Semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                    EMBL/GenBank/DDBJ
          reted (By similarity)
NEUROPILIN IS MEDIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
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                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                 Strowmatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368; DB 1;
No. 1 7e-23;
                                                                                                                                                                                                                                                                                                                                                III) (Sema
                                                                                                                                                                                                                        C
                                                                                                                                                                                                            c.s
of
                                                                                                                                                                                                                                                                                                                                                                                                            771
                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                             transmembrane
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                                                                                                                                                 C
           MEDIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167;
                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                III)
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           ВΥ
                                                                                                                                                                                                             and
           THE
                                                            GROWTH
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                                                                                                                                                                                                            secreted
           CARBOXY
                                                                        GROWTH
                                                            CONES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
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Best Local Sin
Matches 119;
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CARBOHYD
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the content is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR003006; Ig_MHC.
InterPro: IPR003659; Plexin-like.
InterPro: IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00409; IG; 1
SMART; SM00423; PSI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1. Pfam; PF01403; Sema; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L26081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - SIMILARITY:
                                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                           131
                          388
                                                                                                                                                                                                                                                                                                                                      66
                                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                                     32 RLLLVFWVAAASAQGHSRSG----PRISAVWK----GQDHVDF----SQPEPHTVLFHEP
                                                                                                                                                                                                                                                                                                                                                                                            σ
 PVFPM
                                                                                                                          ATN---RNEWRLQDVFLL--PDPSGQWRDTRVYGVF---SNPWNYSAVCVYSLGDIDRVF
                                                                                                                                                                                                                                                  LVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT - - - SDTVMQNPQFIKATIVHQ - DQ
                                                                                                                                                                                                                                                                                                         ER-RGNGLLVCGTNARKPSC------WNLVNDSVVMSLGEMKGYAPFSPDENS
                                                                                                                                                                                                                                                                                                                                     RS-RLYVGAKDHIFSFDLVNIKDFQKIVWPVSYTR---RDECKWAGKDILKECANFIKVL
                          RVEPM
                                                                                                                                                                PEDDKVYFFFRENAIDGEHSGKATHARIGQICKNDFGGHRSL-VNKWTTFLKARLICSVP
                                                                                                                                                                                            AYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDA
                                                                                                                                                                                                                      ASLLIDGELYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPKFISAHLISESDN
                                                                                                                                                                                                                                                                               KAYNQTHLYACGTGAFHPICTYIEIGHHPEDNIFKLENS----HFENGRGKSPYDPKLLT
                                                                                                                                                                                                                                                                                                                                                               GSFSVWVGGRGKVYHFNFPEGKNASVRTVNIGSTKGSCQDK------QDCGNYITLL 130
                                                                                                                                                                                                                                                                                                                                                                                            RIVCLFWGVLLTARANYQNGKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603961;
                                                    LGPYAHRDGPNYQWVPYQGRVPYPRPGTC-PSKTFGGFDSTKDLPDDVITFARSHPAMYN
                                                                                                           GPNGIDTHFDELQDVFLMNFKDP----KNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L26081; AAA65938.1; -. AC004451; AAC06185.1; -. AC004848; AAC78622.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC: 10723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Swiss Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
240
642
727
649
53
125
590
771
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; Glycoprotein
                                                                                -RTSSLKGYHMGLSNPRPGMCLPKK-----QPIPTETFQVADSHPEVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BELONGS TO THE SEMAPHORIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEMA3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590
88889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  771
538
729
769
722
722
125
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%;
28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE C2-TYPE DOMAIN.

ARG/LYS-RICH (BASIC).

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

MW; 9985FBD3EAEDB456 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 363; DB 1; 1
Pred. No. 4.8e-23;
6; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEMAPHORIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                         176
                                                    411
                                                                                                                                                                                             292
                                                                                                                                                                                                                                                                               177
                                                                                                                                                                                                                                                                                                                                     121
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RESULT 6
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SM3B_M
AC Q62177
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DT 30-MAY
DT 16-OCT
DE SEMADAB
MS MUS MUS MUS
MUS MUS
MUS MUS
MUS MUS
CO MAMMAI

RA PUESCH
RT AND AC
RT NEUTON
CC -!- SU
CC -!- SI
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                                                                                      20
                                                                                                                                                                 Query Match
Best Local
                                                                                                                                             Matches
                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the £MBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001627; Sel
Pfam; PF00047; ig; 1.
Pfam; PF01403; Sema; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X85990; CAA59982.1; -. MGD; MGI:107561; Sema3b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS
-:- SUBCELLULAR LOCATION: Secreted (By similarity).
-:- DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE ILEVELS FOUND BETWEEN DAYS 10:12. EXPRESSION PEAKS (MODERATE LEVELS FROM THEN UNTIL BIRTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pueschel A.W., Adams R.H., Betz H.;
"Murine semaphorin D/collapsin is a member of a diverse gene and creates domains inhibitory for axonal extension.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NMRI; TISSUE=Embryo; MEDLINE=95267431; PubMed=7748561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence upon 16-CCT-2001 (Rel. 40, Last annotation upon 16-CCT-2001 (Rel. 40, Last annotation upon 16-CCT-2001)
                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
-!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuron 14:941-948(1995).
-!- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEMA3B OR SEMAA OR SEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q62177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM3B_MOUSE
                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
  46
                                                                                           7 GRAAPSAPRARV--LSLPARFGL-PLRL-----RLLLV----
GHSRSGPRISAVWKGQDHVDFSQPEPHTVLFHEPGSFSVWVGGRGKVYHFNFPEGKNASV 105
                                               GDTAPNLPRLRLSFQELQARHGVRTFRLERTCCYEALLVDEERGRLFVGAENHVASLSLD
                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003659; Plexin-like.
                                                                                                                                                                                                                                  82
124
748
                                                                                                                                                                                                                                                                                                            26
239
636
698
723
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor (Semaphorin
                                                                                                                                                                                                                                       ŘΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                            748
748
536
716
702
743
709
                                                                                                                                                                                                                                       82894 MW;
                                                                                                                                                                 17.1%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain; Multigene family; Neurogenesis; Glycoprotein.
                                                                                                                                           51;
                                                                                                                                                               Score 361.5; DB 1; Pred. No. 6.1e-23;
                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                POLY-GLY.
ARG-RICH (BASIC).
                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                             SEMA
                                                                                                                                                                                                                                                                                                                                                                                                                              SEMAPHORIN
                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                           Mismatches
                                                                                                                                                                                                                                       1866B7D2397C9305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                   3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                             152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>8</u>
                                                                                                                                           Indels 109;
                                                                                                                                                                                     Length 748;
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30-MAY-2000 (Rel. 3
16-OCT-2001 (Rel. 4
Semaphorin 4D precu
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97030273; PubMed-8876214;
Hall K.T., Boumsell L., Schultze J.L., Boussiotis V.A., Dorfman Cardoso A.A., Bensussan A., Nadler L.M., Freeman G.J.;
"Human CD100, a novel leukocyte semaphorin that promotes B-cell aggregation and differentiation.";
Proc. Natl. Acad. Sci. U.S.A. 93:11780-11785(1996).
-!- FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE IMMUNE SYSTEM, AS IN THE NERVOUS SYSTEM. INDUCES B CELLS TO AGGREGATE AND IMPROVES THEIR VIABILITY IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=T-cell;
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Mammalia; Eutheria; Primates;
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SEMA4D OR CD100
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SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.

SIMILARITY: CONTAINS 1 SEMA DOMAIN.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

DATABASE: NAME-PROW; NOTE-CD guide CD100 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd100.htm".

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd100.htm".
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SUBCELLULAR LOCATION: Type I membrane protein
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKE
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL PERIPHERAL BLOOD LYMPHOCYTES, SPLEEN, AND THYMUS AN EXPRESSED AT LOWER LEVELS IN TESTES, BRAIN, KIDNEY,
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InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001627; Sema.
Pfam; PF00047; ig; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFGLPLR----LRLLLVFWVAAASAQGHSRSGPRISAVWKGQDHVDFSQPEPHTVLFHEPG 80
                                 FQVADSHPEVAQRVEPM
                                                                       STAEEVFSHGKYMQSTTVEQSHTKWVRYNGPVPKPRPGACIDSEARAANYTSSLNLPDKT
                                                                                                                                               SFLKARLICSRPDSGLVFNVLRDVFVLRSPG--LKVPVFYALFTPQLNNVGLSAVCAYNL
                                                                                                                                                                                                                       ADVIRKSPDSPDGEDDRVYFFFTEVSVEYEFVFRVLIPRIARVCKGDQGGLRTLQ-KKWT
                                                                                                                                                                                                                                                            ATIVHQD----QAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWN
                                                                                                                                                                                                                                                                                                 PFDPAHSYTSVMVDGELYS---GTSYNFLGSEPIISRNSSHSPLRTEYAIPWLNEPSFVF
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MHC
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27.78;
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N-LINKED (GL
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 361.5;
Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- AVNALNISEKQHEVYWKVSEDKKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ); DB 1;
7.4e-23;
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RESULT 8
SM3A_MOUSE
IN 3A_MOUSE
AC 008665
DT 16-0CT
DT 30-MAY
DT 16-0CT
E(Semab
OS EMBAJA
OS MUS mu
OC ELKRATY
OC MISTIN
RA FEDULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Messersmith c.v., Coodman C.S., Kolodkin A.L.;
Goodman C.S., Kolodkin A.L.;
"Semaphorin III can function as a selective chemorepellent to patter sensory projections in the spinal cord.";
sensory projections in the spinal cord.";
Neuron 14:949-959(1995).

Neuron 14:949-959(1995).

-i- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE. MAY FUNCTION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM3A_MOUSE STANDARD; PRT; 772 AA. 008665; Q62180; Q62215; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Semaphorin 3A precursor (Semaphorin III) (Sem
                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95267432; PubMed=7748562;
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[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=NMRI; TISSUE=Embryo; MEDLINB=95267431; PubMed=7748561; MEDLINB=95267431; PubMed=7748561; Pueschel A.W., Adams R.H., Betz'H.; Pueschel A.W., Adams R.H., Betz'H.; ember of a diverse "Murine semaphorin D/collapsin is a member of a diverse and creates domains inhibitory for axonal extension."; neuron 14:941-948(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEMAJA OR SEMAD OR SEMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kimura T., Fishman M.C.; "cDNA sequence of mouse coll submitted (FEB-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Messersmith E.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 107-772 FROM TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peripheral nerve
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                                                interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                              THIRD OF THE PROTEIN.
SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Secreted.

DEVELOPMENTAL STAGE: EXPRESSED EARLY IN EMBRYONIC D
(E11) IN DISTINCT REGIONS OF THE NEUROECTODERM AND
EXPRESSION BECAME MORE EXTENSIVE AT LATER STAGES.

DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY
                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                          MGI:107558;
                                                                                                                     X85993;
D85028;
L41541;
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                                                                                                   L40484;
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19:519-530(1997).
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                         IPR003599;
IPR003006;
     IPR003659;
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                                                                                                                        BAA19773.1; -. AAL77611.1; -.
                                                                                                                                                                      CAA59985.1; -.
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                                                                            Semaja.
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sa S., Fujisawa
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     Plexin-like.
                            Ig_MHC
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
[1]
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Pfam; PF00047; i
Pfam; PF01403; S
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                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Semaphorin 4B (Semaphorin C) (Sema C)
SEMA4B OR SEMAC OR SEMC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01403; Sema; 1.
SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1.
Signal; Immunoglobulin domain; Multigene
                                          Mus musculus (Mouse)
                                                                                                       SM4B_MOUSE
Q62179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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                                                                                                                                                                    HRDGPNYQWVPYQGRVPYPRPGTC-PSKTFGGFDSTKDLPDDVITFARSHPAMYNPVFPI
                                                                                                                                                                                                         DTHFDELQDVFLMNSKDP----KNPTVYGVFTTSSNTFKGSAVCMYSMSDVRRVFLGPYA
                                                                                                                                                                                                                                                    VYFFFRENAIDGEHSGKATHARIGOICKNDFGGHRSL-VNKWTTFLKARLICSVPGPNGI
                                                                                                                                                                                                                                                             DGELYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDDK
                                                                                                                                                                                                                                                                                                                  GDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQNPQFIKATIV-HQDQAYDDK
                                                                                                                                                                                                                                                                                                                                      QTHLYACGTGAFHPICTYIEVGHHPEDNIFKLQDS---HFENGRGKSPYDPKLLTASLLI
                                                                                                                                                                                                                                                                                                                                                           GNGLLVCGTNARKPSCWNL------VNDSVVMSLGEMKGYAPFSPDENSLVLFE
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                                                                                                                                                                                                                       -RNFNRLQDVFLL--PDPSGQWRDTRVYGVF----SNPWNYSAVCVYSLGDIDRVF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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0047; ig; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA,
                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88799 MW;
                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.9%;
28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC...) (P
D -> N (IN REF. 1).
D -> G (IN REF. 1).
F -> L (IN REF. 1).
F -> L (IN REF. 1).
OH -> EDERGE -> RRSKR (IN REF. 1).
EDERGE -> RRSKR (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARG/LYS-RICH (BASIC).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEMAPHORIN
                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG-LIKE C2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E89A08528B10AEC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                  update)
                                                                                                                 782
                                                              update)
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family;
                                                                                                                                                                                        -QPIPTETFQVADSHPEVAQRVEPM
                                                                                                                 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                  -QDCGNYITLLER-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                    416
                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                  237
                                                                                                                                                                                                                                                                                                                                      182
                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                                                        392
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                                                                                                                                                             Matches
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                         CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X85992; CA/
MGD; MGI:107559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 274:14137-14146(1999).

-i- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXON
-i- SUBUNIT: INTERACTS WITH GIPC PDZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01403; Sema; 1.
Pfam; PF01437; PSI; 1.
SMART; SM00423; PSI; 1.
Transmembrane; Immunoglobulin domain; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pueschel A.W., Adams R.H., Betz H.;
"Murine semaphorin D/collapsin is a member of a diverse gene
and creates domains inhibitory for axonal extension.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99253973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               semaphorin, M-SemF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95267431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTERACTION WITH GIPC
                                      122 DCGNYI-TLLERRGNGLLVCGTNARKPSC-----WNLVND---
  76
                                                                               16
                                                                                                                  72 HTVLFHEPGSFSVWVGGRGKVYHFN----FPEGKNASVRTVNIGSTKGSC--
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDZ protein regulates the distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein. DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE LEVELS FOUND BETWEEN DAYS 10-12. EXPRESSION PEAKS MODERATE LEVELS FROM THEN UNTIL BIRTH. SIMILARITY: BELONGS TO THE SEMADHORIN FAMILY. SIMILARITY: CONTAINS 1 SEMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                           {\tt YTALLLSQDGKTLYVGAREALFALNSNLSFLPGGEYQELLWSADADRKQQCSFKGKDPKR}
DCQNYIKILLPLNSSHLLTCGTAAFSPLCAYIHIASFTLAQDEAGNVILEDG--KGHCPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L.-H., Kalb R.G.,
                                                                                                                                                           104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X85992; CAA59984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14:941-948(1995).
                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001627;
                                                                                                                                                                                                                                     639
782
                                                                                                                                                           Conservative

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663
684
202
548
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555
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471
574

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                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sema4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10318831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=7748561;
                                                                                                                                                                                                                                                                                662
683
782
492
608
726
601
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88
356
471
471
                                                                                                                                                                                                                                         86823 MW;
                                                                                                                                                                          16.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein
                                                                                                                                                           47;
                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                              N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILA
                                                                                                                                                                                                                                         N-LINKED (GLCNAC.
627A81FC8F8F7AC8
                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEMA.
IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY
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(GLCNAC...)
(GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC. .
                                                                                                                                                                                                                                                            (GLCNAC. .
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                                                                                                                                                           138;
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                                                                                                                                                                                                1;
                                                                                                                                                                                                                                         CRC64;
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                                      SVVMSLGEMKGYAPF
                                                                                                                                                           Indels
                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurogenesis;
                                                                                                                                                                                              782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAY 13
                                                                                                                                                         47;
                                                                                                                    ODKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTIW
                                        170
                                                                             75
                                                                                                                    121
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IPR003659;

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RESULT 10
SM3A_RAT
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                                                                    entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM3A_RAT
Q63548;
30-MAY-2000
                                                                                                                               use
                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97073089; PubMed=8915837; Giger R.J., Wolfer D.P., De Wit G.M.J., Verhaagen J.; Giger R.J. wolfer D.P., De Wit G.M.J., Verhaagen J.; "Anatomy of rat semaphorin III/collapsin-1 mRNA expression and relationship to developing nerve tracts during neuroembryogenes J. Comp. Neurol. 375:378-392(1996).
                               InterPro;
                                             EMBL; X95286; CAA64607.1;
                                                                                                                modified
                                                                                                                                                 the
                                                                                                                                                                   between
                                                                                                                                                                                                                     +++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, 30-MAY-2000 (Rel. 39, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEMA3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Semaphorin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229
                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: AT E-11, EXPRESSION WAS RESTRICTED TO THE OLFACTORY PIT, THE BASAL AND ROSTRAL SURFACE OF THE TELENCEPHALIC VESICLE, THE EYE ANLAGE, THE EPITHELIUM OF RATHKE'S POUCH, AND SOMITES. AT LATER DEVELOPMENTAL STAGES, IT WAS WIDELY DISTRIBUTED IN NEURONAL AS WELL AS IN MESENCHYMAL AND EPITHELIAL STRUCTURES OUTSIDE THE NERVOUS SYSTEM. AFTER BIRTH, MESENCHYMAL LEVELS DECREASED RAPIDLY AND EXPRESSION BECAME RESTRICTED TO SPECIFIC SETS OF NEURONS IN THE CAS. IN THE MATURE CNS, IT IS DETECTABLE IN MITRAL CELLS, NEURONS OF THE ACCESSORY BULB AND CEREBRAL CONTEX, CEREBELLAR PURKINJE CELLS, AS WELL AS A SUBSET OF CRANIAL AND
                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                         THIRD OF THE PROTEIN.
SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                    SPINAL MOTONEURONS DOMAIN: STRONG BINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEUROPILIN. Secreted (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGAGE IN THE FORMATION OF SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MAY BE INVOLVED IN GUIDING GROWING AXONS TOWARDS TARGETS BY FORMING A MOLECULAR BOUNDARY THAT INSTRUCTS AXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPNFKSTALVVDGELY-TGTVSSFQGNDPAISRSQSSRPTKTESSLNWLQDPAFVASATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMLVCSDAATNRNFNRLQDVFLL-PDPSGQWRDTRVYGVFSNPWNY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQLLCSRPDDGFPFNVLQDVFTLNPNPQ-DWRKTLSIGVFTSQWHRGTTEGSAICVFTMN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PESLGSPIGDDDKIYFFFSETGQEFEFFENTIVSRVARVCKGDEGGERVLQ-QRWTSFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HQDQAY----DDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLK
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                                                                              an
                                                                              requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                              non-profit institutions as long a and this statement is not removed.
            IPR003599;
IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3A precursor
                                                                                                                                                                                                                                                                                      STRONG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RTSSLKGYHMGLSNPRPGMCL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
            Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
or (Semaphorin III) (Sema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                      ТО
                                                                                                                                                                                                                                                                                    NEUROPILIN IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  772
                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NERVE TRACTS. BINDS
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                                                                                                                                                                                                                                                                                      MEDIATED
                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroembryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               III).
                                                                                                                γď
                                                                                                                                                                                                                                                                                      ВҮ
                                                                                                                and
                                                                                                                                                                                                                                                                                      THE CARBOXY
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Pfam; PF00047; ig; 1. Pfam; PF01403; Sema; 1 SMART; SM00409; IG; 1. SMART; SM00423; PSI; 1

IPR001627;

Sema

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                        090607;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                 _CHICK
MEDLINE-94006554; PubMed-8402908;
Luo Y., Raible D., Raper J.A.;
"Collapsin: a protein in brain the
of neuronal growth cones.";
                                                                                                                   SEMA3A OR COLL1.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                  Semaphorin 3A precursor (Collapsin-1)
                                                                                                                                                                                                       SM3A_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
                                            TISSUE-Brain;
                                                                SEQUENCE
                                                                                    NCBI_TaxID=9031;
                                                                                                        Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Developmental
                                                                                                                                                                                                                                                            358
                                                                                                                                                                                                                                                                                                     302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 VFWVAAASAQGHSRSG----PRISAVWK----GQDHVDF----SQPEPHTVLFHEPGSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWVGGRGKVYHFNFPEGKNASVRTVNIGSTKGSCQDK-----
                                                                                                                                                                                                                                                           HRDGPNYQWVPYQGRVPYPRPGTC-PSKTFGGFDSTKDLPDDVITFARSHPAMYNPVFPI
                                                                                                                                                                                                                                                                                                                VYFFFRENAIDGEHSGKATHARIGQICKNDFGGHRSL-VNKWTTFLKARLICSVPGPNGI
                                                                                                                                                                                                                                                                                                                                                                                      DGELYSGTAADEMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDDK
                                                                                                                                                                                                                                                                                                                                                                                                            GDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQNPQFIKATIV-HQDQAYDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                QTHLYACGTGAFHPICTYIEVGHHPEDNIFKLQDS---HFENGRGKSPYDPKLLTASLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNGLLVCGTNARKPSCWNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFWGILLTARANYANGKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERS-R
                                                                                                                                                                                                                                                                                                                                                                  TYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYVGAKDHIFSFNLVNIKDFQKIVWPVSYTR---RDECKWAGKDILKECANFIKVLKAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                FROM
                                                                                                                                                                                                                                                                      RTSSLKGYHMGLSNPRPGMCLPKK------QPIPTETFQVADSHPEVAQRVEPM
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240
643
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                                                                Ν.Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÃΑ;
                                                                                                                                                                                                       STANDARD;
                                                                                                         Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
772
738
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                                                                AND
                                                                                                                   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.7%;
28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein
                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                    ----KNPIVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYA
    : J.A.;
i brain that
i.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MΚ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEMA.

IG-LIKE C2-TYPE DOMAIN.

ARG/LYS-RICH (BASIC).

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VNDSVVMSLGEMKGYAPFSPDENSLVLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 354;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEMAPHORIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                         Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240907812FF9F2D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                OF.
                                                                                                                                                                      update)
            induces
                                                                322-329;
                                                                                                                                                                                                       772
                                                                                                                                                  update)
(COLL-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163;
            the
                                                                362-372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 772;
           collapse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --QDCGNYITLLER-R
::| |:| :|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                395-403
            and
                                                                                                          Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76;
           paralys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                           416
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Best Local S
Matches 123
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-i- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH CONES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH CONES BY A MOTILITY INHTBITING MECHANISM. BINDS TO NEUROPILIN.

-i- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN BRAIN AND MUSCLE, MODERATE LEVELS IN LUNG, BURSA, AND HEART AND VIRTUALLY ABSENT IN LIVER. COLLAPSIN-1, -2, -3, AND -5 BIND TO OVERLAPPING BUT DISTINCT AXON TRACTS.

-i- DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CARBOXY FILTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001627;
Pfam; PF00047; ig; 1.
Pfam; PF01403; Sema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U02528; AAC59638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
  292
                                                288
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SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THIRD OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                SFSVWVGGRGKVYHFNFPEGKNASVRTVNI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IALLSLGVLLAGRVNCQHVKNNVPRLKLSYKEMLESNNIVNFNGLANSSSYHTFLLDEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRLRLLLVFWVAAASAOGHSRSGPRISAVWK----GQDHVDF----SQPEPHTVLFHEPG
                                           VCSDAATN---RNFNRLQDVFLL--PDPSGQWRDTRVYGVF---SNPWNYSAVCVYSLGD
                                                                                                                                                                                                                                                                                                                                              NYITLLER-RGNGLLVCGTNARKPSCWNL------VNDSVVMSLGEMKGYAPFS
                                                                                                                                                                                                                                                                                                                                                                                                    S-RLYVGAKDHIFSFNL----
                                                                                                                                                                                                PKLLTASLLVDGELYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPRFISAHLI
                                                                                                                                                                                                                                               PDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT - - - SDTVMQNPQFIKATIV
                                                                                                                                                                                                                                                                                                  NFIKVLKTYNQTHLYACGTGAFHPMCTYIEVGSHPEDNIFRMEDS---HFENGRGKSPYD
ICSVPGPNGIDTHFDELQDVFLMNSKDP----KNPIVYGVFTTSSNIFKGSAVCMYSMTD
                                                                                                                                -HQDQAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAML
                                                                                               {\tt PESDNPEDDKIYFFFRENAIDGEHTGKATHARIGQICKNDFGGHRSL-VNKWTTFLKARL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; IPR003599; Ig.
; IPR003006; Ig_MHC.
; IPR003659; Plexin-
; IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003599;
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88867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain; Multigene Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56;
                                                                                                                                                                                                                                                                                                                                                                                                 ----VNIKEYQKIVWPVSHSRRDECKWAGKDILRECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 350; DB 1;
Pred. No. 6.1e-22;
6; Mismatches 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARG/LYS-RICH (BASIC).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL);
E91E09DE0CC940AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEMAPHORIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE C2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               -GSTKGSCQ----DKQDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                  172
                                                                                                                                                                                                                                                                                                                                                                                                 115
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347
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STATE TO THE TENT OF THE PROPERTY OF THE PROPE
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SZ1A_BRARE
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  Query Match
                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertactinopterygii; Neopterygii; Teleostei; Ostaccyprinidae; Danio.
                                                                                                            CARBOHYD
                                                                                                                                     DISULFID
                                                                                                                                                       DOMAIN
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                  Developmental
                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1. Pfam; PF01403; Sema;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; InterPro; IPR003659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99313409; PubMed=10386838; Yee C.S., Chandrasekhar A., Hallor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Embryo;
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Semaphorin z1a precursor (Semaphorin 1A) (Sema-Z1A).
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuwada J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular cloning, expression, and activity of zebrafish semaphorin
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                                                                                                                                                                                                                                                                                                           SM00409; IG; :
SM00423; PSI;
                                                                                                                                                                                                                                                                                         Immunoglobulin
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CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN
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                                               MW;
                                           ; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniform
    Score
                                                                                                                                                     IG-LIKE C2-TYPE DOMAIN. ARG/LYS-RICH (BASIC).
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15-JUN-2000 (Rel. 39, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Semaphorin Z7 precursor (Semaphorin 7)
SEMAZ7 OR SEMA7.
Brachvdanic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _BRARE
SMZ7_BRARE
          EMBL; AF073289; AAC72345.1; ZFIN; 2DB-GENE-990715-7; sen
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
MEDLINE=99060909; PubMed=9867349;
MC., Severance S.M., Yee C.
                                                                                     modified
                                                                                                                                                                                                                                        Mech.
                                                                                                                                                                                                                                                                                                                                            Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                      or send
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                                                                                                                                                                                                                                                      semaphorins
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Cyprinidae; Danio
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                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YAVFTTSSNIFRGSAICMYSMADIRRVF----LGPYAHRDGPNYQWVPFQGRVPYPRPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGDQGGESSLSYSKWNTFLKAMLYCSDAATN---RNFNRLQDVFLL--PDPSGQWRDTRV
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                                                                                                                                                                                                                                        Dev.
                                                      non-profit institutions as long d and this statement is not removed services a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        76:165-168(1998).
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5; Mismatches 155;
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                                                                    (See http://www.isb-sib.ch/announce/
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novel zebrafish
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RESULT 14

SZ1B_BRARE

ID SZ1B_BRARE

AC Q9W686;
DT 30-MAY-2000

DT 15-JUN-2002

DE Semaphorin;
GN SEMAZ1B OR;
OC Eukaryota;
OC Actinoptery;
OC Cyprinidae;
OX NCBI_TAXID=

RN [1]
     Ogw686;

1 30-MAY-2000 (Rel. 39, Created)

T 30-MAY-2000 (Rel. 39, Last sequence update)

T 15-JUN-2002 (Rel. 41, Last annotation update)

E Semaphorin ZIB precursor (Semaphorin IB) (Sema-/)

S EMAZIB OR SEMAJAB.

S Brachydanio rerio (Zebrafish) (Danio rerio).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebro CC Actinopterygii; Neopterygii; Teleostei; Ostario CC Cyprinidae; Danio.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Trans Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
                                                                                                                                                                                                          391
                                                                                                                                                                                                                                                                                                                                                     216
                                                                                                                                                                                                                                                                                                                                                                                                   161
                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 LFREEG---IWNYTTMLLRDDLNLLILGAREAIFALDLDDITIKKAMLKWEVTRDQQNDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 LEHEPGSESVW------VGGRGKVYHENEPE--GKNASVRTVNIGSTKGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; PF01403; Sema; 1.
; PF01437; PSI; 1.
T; SM00410; IG_like; 1
T; SM00423; PSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDK-----QDCGNYITLLERRGNG-LLVCGTNARKPSCWNLVNDSVVMSL----GEMKGY
                                                                                                                                                                                                          DKTLQFVKDKPLMDQAVTAEQP 412
                                                                                                                                                                                                                                 TETFQVADSHPEVAQRVEPMGP 394
                                                                                                                                                                                                                                                       YKIEDIKTVFSKGKFKAPFNVETSFVKWVMYSGELPDPRPGACIDNHAREKGITKSLELP
                                                                                                                                                                                                                                                                               YSLGDIDRVFRTSSLKG------
                                                                                                                                                                                                                                                                                                      WTSFLKARLDCQVPNTNLPL-LVQDVFHLCPD---DWTTCVFYAVFTPQSDSSQYSAVCS
                                                                                                                                                                                                                                                                                                                            WNTFLKAMLVCSDAATNRNFNRLQDVF-LLPDPSGQWRDTRVYGVF---SNPWNYSAVCV
                                                                                                                                                                                                                                                                                                                                                   IHMAHIPEGQSNPDGDDDKIYLFFSETAVEYESYTKVDVSRVARVCKGDLGGQRTLQ-KK
                                                                                                                                                                                                                                                                                                                                                                   IKATIVHQDQAY----DDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSK
                                                                                                                                                                                                                                                                                                                                                                                                  CPFDPFQRYTSAMV----DGAYYSATSMNFRGSEPVMMRSTEESIRTEFTS-
                                                                                                                                                                                                                                                                                                                                                                                                                         APFSPDE---NSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGES--ELYTSDTVMQNPQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNKGKDATNDCKNYIRILHKKNDGRMYVCGTKAFNPTCGYLSYADGKLTLEILQEDTKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002165;
IPR001627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
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665
686
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577
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532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ig; 1.
Sema;
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
766
664
685
766
766
522
522
630
623
633
633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.2%;
29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plexin_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plexin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC ,

SEMA.

IG-LIKE C2-TYPE DOMAIN.

BY STMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

(GLCNAC. . .) (POTENTIAL).

(GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEMAPHORIN 27.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
SEMA.
SEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 344.5;
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ed. No. 1.8e-21;
Mismatches 146;
                                                                                                                                                                                                                                                                              -YHMGLSNPRPGMC-----LPKKQPIP
                                                                                                                                              778
                                     Ostariophysi;
                                               Vertebrata;
                                                                                  (Sema-Z1B).
                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                   TWLSEPNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                    274
                                                                                                                                                                                                                                                                                                                                                                            278
                                                                                                                                                                                                                                                                                                                                                                                                                         222
                                                                                                                                                                                                                                                                                                                                                                                                                                                  160
                                                                                                                                                                                                                                                                                                                                                                                                  215
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                                                      Db
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                                                                                                             В
                                                                                                                                                                                                δÃ
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                                                                                                                                                                                                                                                         γ
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002165; InterPro; IPR001627; InterPro; IPR001627; Ipfam; PF00047; Ig; 1. pfam; PF01403; Sema; Jefam; PF01437; PSI; 1.
                                                                                                                                                                                                                                                                                                                                              DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Zebrafish semaphorin 71b inhibits growing motor axons i mech. Dev. 87:103-117(1999).

-i- FUNCTION: MIGHT NORWALLY INFLUENCE THE MIDSEGMENTAL OF THE VENTRALLY EXTENDING MOTOR AXONS BY CONTRIBUTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF083382; AAD28103.1; -.
ZFIN; ZDB-GENE-991209-6; sema3ab.
InterPro; IPR003599; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=99425174; PubMed=10495275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Immuno
Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003659; Plexin-like
237
                         231
                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                         33 LLLVFWVAAASAQG----HSRSG-PRISAVWK----GQDHVDF----SQPEPHTVLFHEP
                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPULSIVE DOMAIN IN THE POSTERIOR SOMITE.
SUBCELLULAR LOCATION: Secreted (By similarity).
TISSUE SPECIFICITY: EXPRESSED IN RHOMBOMERES THREE AND FIVE, AN IN THE POSTERIOR HALF OF NEWLY FORMED SOMITES WHICH IS AVOIDED VENTRALLY EXTENDING MOTOR AXONS.
SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C3-TYPE DOMAIN.
             DQAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS
                                                                                                                                                                                                                              IVLLIWTLIAPERGTVAQRSKSNVPRLKPSYKEMLESNNLLTFNGLANSSAYHTFLLDEE
DNAEDDKIYLFFRENAIDGEQISKATHARIGQLCKNDFGGHRSL-VNKWTTFLKARLVCS
                                                       TASMLIDG
                                                                                 NSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT - - - SDTVMQNPQFIKATIV - HQ
                                                                                                               NF TKVLQPFNQTHLYACGTGAFHPVCAHVEVGKRSEDNTFRLGSSFENGRGKSPYDPKLQ
                                                                                                                                          NYITLLER-RGNGLLVCGTNARKPSCWNLV----NDSVVMSLGEM----KGYAPFSPD-E
                                                                                                                                                                     RG-RLFVGAKDHVLSFNLVD-----INMDQQLISWPSSPSRRDECKWAGKDVQKECA
                                                                                                                                                                                                GSFSVWVGGRGKVYHFNFPEGKNASVRTVNIG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00409; IG; 1
SM00423; PSI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin mental protein;
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                              18
241
645
721
652
652
54
127
593
778
                                                                                                                                                                                                                                                                                       Conservative
                                                      -ELYAGTSADFMGRDFAIFRTLGKHHPIRTEQHDSRWLNDPRFVSVHLIPES
                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                           778
539
723
776
716
716
127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plexin_repeat.
                                                                                                                                                                                                                                                                                                    16.2%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain; Multigene family; Neurogenesis;
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY. . . . . (PO'

N-LINKED (GLCNAC. . . ) (PO'
                                                                                                                                                                                                                                                                                                    Score 342.5; DB 1
Pred. No. 2.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE C2-TYPE DOMAIN. ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEMAPHORIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z1B.
                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                       152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONTRIBUTING
                                                                                                                                                                                                 STKGSCQ - - - I- - DKQDCG
                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŗ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY CHOICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vivo
                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
                           290
                                                                                                               177
                                                                                                                                           174
                                                                                                                                                                      117
                                                                                                                                                                                                   124
                                                                                                                                                                                                                              66
295
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RESULT 15
VA39_VAGCV
ID VA39_VAGCV
ID VA39_VAGA
DT 01-MAR
OC Orthop
OX Vaccin
OC Orthop
OX NCBL_T
RN [1]
RP SEQUEN
RA Amegad
RT "Ident
RT "Ident
RT "Ident
RT "SEQUEN
RA Amegad
RT "Ident
RT "Ident
RT "Nucle
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RL J. Gen
CC ----
RL D. RE
CC ----
RL D. RE
CC ----
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CC ----
CC modifi
CC ----
DR EMBL;
DR EMBL;
DR EMBL;
DR EMBL;
DR FABM;
SQ SEQUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                          EMBL; M61187; AAA48335.1; -. EMBL; D11079; BAA01811.1; AI EMBL; X57318; CAA40587.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91259063; PubMed-2045793; Smith G.L., Chan Y.S., Howard S.T.; "Nucleotide sequence of 42 kbp of vaccinia virus strain WR from the right inverted terminal repeat."; J. Gen. Virol. 72:1349-1376(1991).
-!- CAUTION: IN REF.2 THIS SEQUENCE IS IN TWO PART (SALL9R AND SALFIR) DUE TO THE PRESENCE OF FRAMESHIFT COMPARED TO THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-91310644; PubMed-1856205; Ann B. Y., Moss B.; Amegadaie B.Y., Ahn B. Y., Moss B.; and the gene encoding a Mr "Identification, sequence, and expression of the gene encoding a Mr 35,000 subunit of the vaccinia virus DNA-dependent RNA polymerase."; J. Biol. Chem. 266:13712-13718(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccinia virus (strain Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
protein A39.
A39R OR SALL9R/SALFIR.
                                           118
                                                                                                                                                                                                                                                                                     NBL; A2/21, S29921.
VIR; S29921; S29921.
EnterPro; IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10254;
                                                                              141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P24764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VA39_VACCV
     201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291
                                                                                                              74 LYTGVNGAVYTES----NNKLNKT---GLTN-----NNYITTSIKVEDADKDTLVC 117
                                                                                                                                                 84 VWVGGRGKVYHFNFPEGKNASVRTVNIGSTKGSCQDKQDCGNYITL---LERRGNGLLVC 140
                                                                                                                                                                                                                Local Similarity
                                                              GTNARKPSCWNLVNDSVVMSLGEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPR 200
FRRIRGES--ELYTSDTVMQNPQFIKATIVHQDQAYDDKIYYFFREDNPDKNPEAPLNVS 258
                                     GTNNGNPKCWKIDGSDDPKHRG--RGYAPYONSKVTIISHNGC-VLSDINISKEG--IKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPAMYNPVFPI 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPGLNGIDTHFDELQDVFLMSSKDP----KNPITYAVFTTSSNIFKGSAVCMYSMADIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPEVAORVEPM 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VF----LGPYAHRDGPNYQWVPFLNRVPYPRPGTC-PSKTFDGFESTKDFPDDVITFARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFRTSSLKGY-HMGLSN------PRPGMCLPKK-----QPIPTETFQVADS
                                                                                                                                                                                                                                                                     PF01403; Sema;
NCE 441 AA; !
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (strain WR).

(strain WR).

viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                       50185 MW;
                                                                                                                                                                                                              16.1%;
31.1%;
                                                                                                                                                                                                                                                                                                                                                               ALT_SEQ.
                                                                                                                                                                                            51;
                                                                                                                                                                                        Score 341.5; DB 1;
Pred. No. 1.5e-21;
1; Mismatches 127;
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                                                                                                                                                                                                                              Length 441;
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                         VADSHPEVAQRVEPM 392
                                                     ILYVFFDSPYSKSALCTYSMNTIKQSFSTSKLEGYTKQLPSPASGICLPAGKVVPHTTFE
                                                                                  RVYGVFSNPWNYSAVCVYSLGDIDRVFRTSSLKGYHMGLSNPRPGMCLPKKQPIPTETFQ 377
                                                                                                                                         RVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS-DAATNRNFNRLQDVFLLPDPSGQWRDT 317
                                                     34C
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Search completed: March 14, 2003, 09:26:00 Job time: 12.6906 secs